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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : A61K 38/17, C07K 14/705, C12N 15/79, G01N 33/68 — A1

(11) International Publication Number: WO 96/21457

(43) International Publication Date: 18 July 1996 (18.07.96)

(21) International Application Number: PCT/US95/17024

(22) International Filing Date: 28 December 1995 (28.12.95)

(30) Priority Data:
08/372,217 13 January 1995 (13.01.95) US

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(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
With international search report.

(54) Title: ALLOSTERIC CONTROL OF NUCLEAR HORMONE RECEPTORS

(57) Abstract

Heterodimerization is a common paradigm among eucaryotic transcription factors, though it remains unclear how individual monomers contribute to the overall transcriptional activities of the complex. The 9-*cis* retinoic acid receptor (RXR) serves as a common heterodimerization partner for several nuclear receptors including the thyroid hormone (T_3R), retinoic acid (RAR) and vitamin D receptors. A strategy has been devised to examine the transcriptional properties of each receptor individually or when tethered to a heterodimeric partner. It has been found that the intrinsic activity of RXR is masked in RXR-T_3R and RXR-RAR heterodimers. In contrast, a novel RXR-Nurr1 heterodimer described herein is highly responsive to RXR ligands, suggesting that different partners exert unique allosteric control over the RXR response. These findings establish a novel 9-*cis* retinoic acid response pathway and resolve the paradox as to how T_3R, RAR and VDR contribute to distinct physiologic pathways while sharing a common RXR subunit.

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WO 96/21457 PCT/US95/17024

Allosteric Control of Nuclear Hormone Receptors

Field of the Invention

The present invention relates to intracellular receptors, and methods for the modulation thereof. In a particular aspect, the present invention relates to novel heterodimeric complexes. In another aspect, the present invention relates to methods for modulating processes mediated by retinoid X receptor and/or orphan receptor Nurr1.

Background of the Invention

Heterodimerization is a common theme in eucaryotic regulatory biology. Indeed, a number of transcription factor families have been defined by their characteristic dimerization interface. These include the leucine zipper (e.g. fos, jun, CREB, C/EBP; see, for example, Lamb and McKnight, in *Trends Biochem. Sci.* 16:417-422 (1991)), helix-loop-helix (e.g. myc, max, MyoD, E12, E47; see, for example, Amati and Land, in *Curr. Opin. Genet. Dev.* 4:102-108 (1994)), rel (NFκB, dorsal; see, for example, Blank et al., in *Trends Biochem. Sci.* 17:135-140 (1992)), ankyrin (GABP; see, for example, Brown and McKnight, in *Genes Dev.* 6:2502-2512 (1992)), and the nuclear receptor superfamilies (see, for example, Evans, in *Science* 240:889-895 (1988), and Forman and Samuels, *Mol. Endocrinol.* 4:1293-1301 (1990)). Detailed analyses of these proteins have shown that heterodimerization produces novel complexes that bind DNA with higher affinity or altered specificity relative to the individual members of the heterodimer (see, for example, Glass, in *Endocr. Rev.* 15:391-407 (1994)). Indeed, little is known about the contributions of each monomer toward the transcriptional properties of the complex.

Nuclear hormone receptors are characterized by a central DNA binding domain (DBD) ~~see Figure 1)~~, which targets the receptor to specific DNA sequences, known as hormone response elements (HREs). The retinoic acid receptor (RAR), the thyroid hormone receptor (T_3R), the vitamin D_3 receptor (VDR) and the fatty acid/peroxisome proliferator activated receptor (PPAR) preferentially bind to DNA as heterodimers with a common partner, the retinoid X (or 9-*cis* retinoic acid) receptor (RXR; see, for example, Yu et al., in *Cell* 67:1251-1266 (1991); Bugge et al., in *EMBO J.* 11:1409-18 (1992); Kliewer et al., in *Nature* 355:446-449 (1992); Leid et al, in *Cell* 68:377-395 (1992); Marks et al., in *EMBO J.* 11:1419-1435 (1992); Zhang et al., in *Nature* 355:441-446 (1992); and Issemann et al., in *Biochimie*. 75:251-256 (1993).

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Naturally occurring HREs are composed of direct repeats (i.e., DRs; see Umesono et al., in *Cell* 65:1255-1266 (1991), inverted repeats (i.e., IRs; see Umesono et al., in *Nature* 336:262-265 (1988), and Williams et al. in *J. Biol. Chem.* 266:19636-19644 (1991)), and/or everted repeats (ERs; see Baniahmad et al., in *Cell* 61:505-514 (1990); Farsetti et al., in *J. Biol. Chem.* 267:15784-15788 (1992); Raisher et al., in *J. Biol. Chem.* 267:20264-20269 (1992); or Tini et al., in *Genes Dev.* 7:295-307 (1993)) of a degenerate X_n-AGGTCA core-site.

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The DNA binding domain (DBD) contains two helical regions, one of which serves as a recognition helix that makes base-specific contacts within the major groove of the core-site (see, for example, Luisi et al., in *Nature* 352:497-505 (1991) and Schwabe et al., in *Cell* 75:567-578 (1993)). A third helix has been identified in some receptors which makes additional minor groove contacts in the 5' portion of the core-binding site, X_n (see, for example, Wilson et al., in *Science* 256:107-110 (1992) or Lee et al., in *Science* 260:1117-1121 (1993)).

In direct repeats (DR, head-to-tail arrangement), the X_n sequence also serves as a gap which separates the two core-binding sites. Spacers of 1, 3, 4 and 5 nucleotides serve as preferred response elements for heterodimers of RXR with PPAR, VDR, T_3R and RAR, respectively (see, for example, Naar et al., in *Cell* 65:1267-1279 (1991); Umesono et al., 1991, supra; Kliewer et al., in *Nature* 358:771-774 (1992); and Issemann et al., supra). The optimal gap length for each heterodimer is determined by protein-protein contacts which appropriately position the DBDs of RXR and its partner (see, for example, Kurokawa et al., in *Genes Dev.* 7:1423-1435 (1993); Perlmann et al., in *Genes Dev.* 7:1411-1422 (1993); Towers et al., in *Proc. Natl. Acad. Sci. USA* 90:6310-6314 (1993); and Zechel et al., in *EMBO J.* 13:1414-1424 (1994)). In contrast to this mode of DNA binding, a growing number of receptor-like proteins have been identified which bind as a monomer to a single core-site. The NGFI-b/Nurr1 orphan receptors provide well characterized examples of this paradigm (Wilson et al., in *Mol. Cell Biol.* 13:5794-5804 (1993)).

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Once bound to an HRE, each receptor responds to its signal through the C-terminal ligand binding domain (LBD), which binds its cognate hormone with high affinity and specificity (see, for example, Evans, 1988, supra; or Forman and Samuels, 1990, supra). The LBD is a complex entity containing several embedded subdomains. These include a C-terminal transactivation function ($\tau 2$), a series of heptad repeats which serve as a dimerization interface and a poorly-delineated transcriptional suppression domain (see Figure 1, and Forman and Samuels, 1990, supra).

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The transactivation domain, $\tau 2$, consists of approximately 20 amino acids with the potential to form an amphipathic α-helix (see Zenke et al., in *Cell* 61:1035-1049 (1990); Danielian et al., in *EMBO J.* 11:1025-1033 (1992);

Nagpal et al., in *EMBO J.* 12:2349-2360 (1993); and Durand et al., in *EMBO J.* 13:5370-5382 (1994)). When linked to a heterologous DNA binding domain, the isolated τ2 domain displays constitutive transcriptional activity. However, in the natural context of the LBD, transcriptional activity requires the addition of ligand.

The above-described evidence indicates that the LBD functions as a modular unit whose transcriptional activities are controlled by ligand. Accordingly, it should be possible for both members of a receptor heterodimer to be simultaneously activated by specific ligands therefor. However, in spite of this possibility, it has been discovered that the ligand-induced transcriptional activities of various receptor subtypes vary as a function of the partner with which a subtype participates in the formation of a heterodimer. For example, the ligand-induced transcriptional activities of RXR are suppressed when complexed with RAR and T_3R. This suppression occurs at the level of ligand binding and transcriptional activation. Furthermore, RXR responsiveness has not been observed with other partners, including VDR.

Accordingly, the identification of receptor subtypes which participate in the formation of RXR-containing heterodimers, yet retain the ability to be activated by RXR-selective ligands, would be highly desirable. The present invention identifies such receptor subtypes and provides methodology for identifying additional receptor species having such properties.

Brief Description of the Invention

In accordance with the present invention, it has been discovered that RXR can interact productively with Nurr1, a member of the nuclear receptor superfamily that

(in the absence of heterodimerizing partner therefor) is capable of binding DNA as a monomer (see, for example, Law et al., in *Mol. Endocrinol.* 6:2129-2135 (1992); and Scearce et al., in *J. Biol. Chem.* 268:8855-8861 (1993)). As a result of this interaction, the constitutive activity of Nurr1 is suppressed, and the resulting complex becomes responsive to RXR-selective ligands (e.g., 9-*cis* retinoic acid). The unique ability of the Nurr1-RXR heterodimer complex to transduce RXR signals establishes a novel response pathway.

The results described herein suggest that heterodimer formation imparts allosteric changes upon the ligand binding domain (LBD) of nuclear receptors. These allosteric changes confer transcriptional activities onto the heterodimer that are distinct from those of the component monomers. This arrangement permits a limited number of regulatory proteins to generate a diverse set of transcriptional responses to multiple hormonal signals.

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Brief Description of the Figures

Figure 1 schematically represents the functional domains of nuclear hormone receptors. "DNA" represents the DNA binding domain. "LIGAND" reprsents the large C-terminal ligand binding domain. Dimerization and transactivation (τ2) functions are embedded within this region, as illustrated.

Figure 2 illustrates the differential modulation of RXR response by T_3R (shown in Figure 2A) and RAR (shown in Figure 2B).

Figure 3 illustrates the differential modulation of RXR transcriptional activity by the LBDs of T_3R, RAR and VDR.

Figure 4A illustrates the differential modulation of RXR transcriptional activity by the LBD of T_3R, wherein cells treated according to Figure 3 were additionally treated with T_3 (i.e., T_3R ligand) and LG69 (i.e., an RXR specific ligand). Normalized reporter activity was determined and plotted as fold-activation relative to untreated cells.

Figure 4B illustrates the differential modulation of RXR transcriptional activity by the LBD of RAR, wherein cells treated according to Figure 3 were additionally treated with AM580 (i.e., an RAR specific ligand) and LG69. Normalized reporter activity was determined and plotted as fold-activation relative to untreated cells.

Figure 5 illustrates the ability of T_3R and RAR to suppress transcription of a constitutively active RXR derivative (i.e., VP16-RXR).

Figure 6 collectively illustrates that the ligand binding acvitivy of RXR is altered by T_3R and RAR.

Figure 6A illustrates the binding of LG69 (an RXR specific ligand), at-RA (all-trans retinoic acid, an RAR specific ligand) and Am580 (an RAR specific ligand) to RXR and/or RAR.

Figure 6B illustrates that the binding of LG69 to RXR is reduced in RAR-RXR and T_3R-RXR heterodimers.

Figure 6C illustrates that competition of [^{3}H]9-cis RA bound to RXR-RAR heterodimers requires RAR and RXR ligands.

Figure 7 collectively demonstrates that a novel Nurr1-RXR complex provides a signaling pathway for 9-cis retinoic acid.

Thus, Figure 7A presents the results of transient transfection analysis of GAL-Receptor LBD chimeras in the presence of the RXR LBD.

Figure 7B presents transient transfection analysis of full-length Nurr1 and/or RXR.

Figure 7C presents a comparison of the responsivity of Nurr1-RXR complex, or RXR alone, in the presence and absence of RXR specific ligand in the presence of a Nurr1 specific response element (NBRE) or an RXR specific response element (CRBPII).

Figure 7D demonstrates that the RXR LBD activates through Nurr1 but inhibits activation of other receptors.

Figure 8 presents an allosteric control model of ligand responsiveness.

Detailed Description of the Invention

In accordance with the present invention, there is provided a heterodimer complex comprising RXR and a silent partner therefor.

As employed herein, the term "silent partner" refers to members of the steroid/thyroid superfamily of receptors which are capable of forming heterodimeric species with RXR, wherein the silent partner of the heterodimer is not capable of binding ligand (i.e., only the RXR co-partner of the heterodimer is capable of binding ligand).

As employed herein, the phrase "members of the steroid/thyroid superfamily of receptors" (also known as "nuclear receptors" or "intracellular receptors") refers to hormone binding proteins that operate as ligand-dependent

transcription factors, including identified members of the steroid/thyroid superfamily of receptors for which specific ligands have not yet been identified (referred to hereinafter as "orphan receptors"). These hormone binding proteins have the intrinsic ability to bind to specific DNA sequences. Following binding, the transcriptional activity of target gene (i.e., a gene associated with the specific DNA sequence) is modulated as a function of the ligand bound to the receptor.

The DNA-binding domains of all of these nuclear receptors are related, consisting of 66-68 amino acid residues, and possessing about 20 invariant amino acid residues, including nine cysteines.

A member of the superfamily can be identified as a protein which contains the above-mentioned invariant amino acid residues, which are part of the DNA-binding domain of such known steroid receptors as the human glucocorticoid receptor (amino acids 421-486), the estrogen receptor (amino acids 185-250), the mineralocorticoid receptor (amino acids 603-668), the human retinoic acid receptor (amino acids 88-153). The highly conserved amino acids of the DNA-binding domain of members of the superfamily are as follows:

Cys - X - X - Cys - X - X - Asp* - X -
Ala* - X - Gly* - X - Tyr* - X - X -
X - X - Cys - X - X - Cys - Lys* -
X - Phe - Phe - X - Arg* - X - X - X -
X - X - X - X - X - X - (X - X -) Cys -
X - X - X - X - X - (X - X - X -) Cys -
X - X - X - Lys - X - X - Arg - X - X -
Cys - X - X - Cys - Arg* - X - X -
Lys* - Cys - X - X - X - Gly* - Met
(SEQ ID No 1);

wherein X designates non-conserved amino acids within the DNA-binding domain; the amino acid residues denoted with an asterisk are residues that are almost universally conserved, but for which variations have been found in some identified hormone receptors; and the residues enclosed in parenthesis are optional residues (thus, the DNA-binding domain is a minimum of 66 amino acids in length, but can contain several additional residues).

Examples of silent partners contemplated for use in the practice of the present invention are various isoform(s) of Nurr1, HNF4 [see, for example, Sladek et al., in Genes & Development 4: 2353-2365 (1990)], the COUP family of receptors [see, for example, Miyajima et al., in Nucleic Acids Research 16: 11057-11074 (1988), Wang et al., in Nature 340: 163-166 (1989)], COUP-like receptors and COUP homologs, such as those described by Mlodzik et al., in Cell 60: 211-224 (1990) and Ladias et al., in Science 251: 561-565 (1991), the ultraspiracle receptor [see, for example, Oro et al., in Nature 347: 298-301 (1990)], and the like.

RXR species contemplated for use in the practice of the present invention are selected from RXRα, RXRβ, RXRγ, and the like.

In accordance with another embodiment of the present invention, there is provided a method to suppress the constitutive activity of Nurr1. Such method comprises contacting Nurr1 with at least the ligand binding domain of RXR.

In accordance with yet another embodiment of the present invention, there is provided a method to render Nurr1-containing cells inducibly responsive to RXR selective ligands. Such method comprises contacting such cells with at least the ligand binding domain of RXR.

In accordance with still another embodiment of the present invention, there is provided a method to render RXR-containing cells responsive to RXR selective ligands. Such method comprises contacting said cells with a silent partner therefor.

In accordance with a further embodiment of the present invention, there is provided a method for the identification of nuclear receptor(s) which participate as silent partner(s) in the formation of a heterodimer with RXR. Such method comprises

introducing into a cell:

at least the ligand binding domain of a putative silent partner for RXR,

a chimeric construct containing a GAL4 DNA binding domain and at least the ligand binding domain of RXR, and

a reporter construct, wherein said reporter construct comprises:

(a) a promoter that is operable in said cell,

(b) a GAL4 response element (or a response element for the putative silent partner, when substantially full length putative receptor is employed), and

(c) DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said GAL4 response element is operatively linked to said promoter for activation thereof, and thereafter

monitoring expression of reporter upon exposure of the above-described cell to RXR selective ligand(s).

In accordance with a still further embodiment of the present invention, there is provided a method for identifying ligands selective for heterodimers comprising RXR and a silent partner therefor. Such method comprises

comparing the level of expression of reporter when cells containing a reporter construct, RXR and silent partner therefor are exposed to test compound, relative to the level of expression of reporter when cells containing a reporter construct, RXR and a member of the steroid/thyroid superfamily which is not a silent partner therefor are exposed to test compound, and

selecting those compounds which activate only the combination of RXR and silent partner therefor.

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The LBD of nuclear hormone receptors is a complex multifunctional unit containing subdomains for dimerization, transcriptional suppression and hormone-induced transactivation (Forman and Samuels, 1990, supra). The dimerization domain incudes a series of heptad repeats flanked by sequences required for ligand binding. Thus, the dimerization domain is embedded within the larger LBD. This structural arrangement raises the possibility that dimerization may serve as an allosteric modulator of ligand binding and transactivation. This possibility has been investigated with the following observations.

First, dimerization within the LBD is utilized to confer transcriptional suppression upon certain heterodimeric complexes. This is exemplified by unliganded T_3R and RAR, which confer transcriptional suppression upon RXR. Similarly, in accordance with the present invention, it is demonstrated that RXR can suppress constitutive activation by Nurr1.

Second, the intrinsic ligand binding capacity of the LBD can be modulated by dimerization. This is illustrated by the ability of unliganded RAR to abrogate

the ligand binding activity of RXR. It has also been found that T_3R induces a similar suppression, but the presence of ligand therefor, i.e., T_3, is required for the complete effect. Thus, RXR is seen to serve as a silent partner when participating in the T_3R and RAR pathways.

However, not all heterodimeric interactions restrict ligand-responsiveness. Indeed, in accordance with the present invention, it is demonstrated that RXR actively confers ligand-responsiveness upon the Nurr1-RXR heterodimer complex. Similarly, it has previously been shown that the *Drosophila* ecdysone receptor (EcR) acquires ligand binding activity after heterodimerization with USP (*Drosophila* homolog of RXR; see Yao et al., in *Nature* 366:476-479 (1993)). Thus, differential interactions among receptor LBDs can either restrict, redirect or lead to an acquisition of new ligand binding phenotypes.

In accordance with the results described herein, a structural model is proposed (see Figure 8) to account for the observations. In Figure 8, RXR (dark shading) and its partner receptor (e.g., T_3R, RAR or Nurr1 (designated "R" in the figure, shown in light shading) initially exist as monomers in solution. RXR in monomeric form is capable of binding ligand. RXR-receptor heterodimers then form, driven by the dimerization interface that is embedded within the ligand binding domain (LBD). Subsequent to dimerization, binding of ligand (e.g., 9-cis RA) to RXR is modestly reduced by T_3R and dramatically reduced by RAR. Addition of ligand for T_3R (e.g., T_3) results in a further reduction in 9-cis RA binding, while certain retinoids (shown as "RA" in the figure) such as Am580 (an RAR specific ligand) may restore 9-cis RA binding to RXR-RAR. It is of particular note that the Nurr1-RXR heterodimer maintains the ability to bind 9-cis RA.

The above-described structural model relies on the observation that a major dimerization interface is embedded within the larger LBD. It is proposed that upon dimerization, the structure of the RXR ligand binding/dimerization domain is altered. Each RXR partner gives rise to unique conformational changes that either maintain or abrogate RXR ligand binding activity. Binding of ligand by the partner receptor induces a conformational change that can be propagated through the dimerization interface onto the LBD of RXR. This model allows one to explain how the dimerization partner and its specific ligand exert allosteric control over the RXR ligand response.

In the above-described model, the RXR monomer (or homodimer) is capable of binding ligand with high affinity. When RXR interacts with one of its non-permissive partners (i.e., T_3R or RAR), its ability to bind ligand is diminished. On the other hand, dimerization of USP/RXR with EcR promotes high affinity binding of ecdysone to EcR. It is believed that these effects are a direct consequence of the localization of a major dimerization interface within the LBD (see Figures 1 and 8). The above-described model predicts that this structural arrangement serves to functionally link dimerization and ligand binding activities. This would then provide a mechanism by which dimerization could exert allosteric control over the ligand response.

In addition to dimerization, ligand binding by one receptor may also result in allosteric modification of its partner. Specifically, binding of ligand to the RXR partner can either restore (as in the case of RAR) or further decrease (as in the case of T_3R) the ligand binding potential of RXR (see Figure 6). It is already known that upon ligand binding the cognate receptor undergoes a conformation change (see, for example, Toney et al., in

Biochemistry 32:2-6 (1993)). The results provided herein support the suggestion that ligand-induced conformation changes in the LBD of one heterodimer partner will be propagated through the dimerization interface onto the LBD of the partner. Thus, the model presented above can explain how a dimerization partner and its specific ligand can exert allosteric control over the RXR ligand response. Similarly, the above-described model can account for the ability of ligand to either promote EcR-USP, (Yao et al., 1993, supra) or destabilize VDR-RXR and T_3R-T_3R dimers (see, for example, Andersson et al., in *Nucleic Acids Res.* 20:4803-4810 (1992); Ribiero et al., in *Mol. Endocrinol.* 6:1142-1152 (1992); Yen et al., in *J. Biol. Chem.* 267:3565-3568 (1992); MacDonald et al, in *Mol. Cell Biol.* 13:5907-5917 (1993); and Cheskis and Freedman, in *Mol. Cell Biol.* 14:3329-3338 (1994)).

The restriction of RXR activity within certain heterodimers indicates that 9-*cis* RA responsiveness is not an obligatory consequence of heterodimerization with RXR. This allows RXR to function as both a receptor and as a heterodimerization partner, without requiring all target genes to be 9-*cis* RA responsive. This explains the paradox as to how RXR serves as a common subunit for receptors which display independent physiologic effects (e.g. T_3R, RAR, VDR).

In contrast, the ability of RXR to transduce signals when complexed with Nurr1 suggests an alternative pathway for 9-*cis* RA signaling. Nurr1 expression is induced by physiological stimuli (see Davis and Lau, in *Mol. Cell Biol.* 14:3469-3483 (1994)) including membrane depolarization and liver regeneration (Scearce et al., 1993, supra). Based on the results presented herein, it is clear that RXR contributes to the regulation of these events.

Unlike previously described heterodimers, RXR functionally interacts with Nurr1 in the absence of RXR-specific DNA contacts (see Figure 7D). Indeed, the ability to tether to a DNA bound monomer is a distinguishing feature of the Nurr1-RXR heterodimer complex. As a result, an RXR mutant that is deficient in DNA binding activates through Nurr1 while it inhibits other receptor heterodimers (see Figure 7D).

In accordance with the present invention, there are provided methods for the modulation of Nurr1 expression induced by physiological stimulus of a subject. Such method comprises administering to the subject an effective amount of a composition comprising at least the ligand binding domain of RXR. Physiological stimuli contemplated for treatment in accordance with the present invention include any event which induces production of calcium ions, cyclic AMP, ACTH, and the like.

The invention will now be described in greater detail by reference to the following non-limiting examples.

Example 1
Cell Culture and Transfection

CV-1 cells were grown in Dulbecco's Modified Eagle's medium supplemented with 10% resin-charcoal stripped (Samuels et al., *Endocrinology* 105:80-85 (1979)) fetal bovine serum, 50 U/ml penicillin G and 50 μg/ml streptomycin sulfate (DMEM-FBS) at 37°C in 5% CO_2. One day prior to transfection, cells were plated to 50-80% confluence using phenol-red free DMEM-FBS. Cells were transfected by lipofection using N-(2-(2,3)-dioleoyloxy)propyl-N,N,N-trimethyl ammonium methyl sulfate) according to the manufacturer's instructions (DOTAP, Boehringer Mannheim). After 2 hours, the liposomes were removed and cells treated for 40 hours with phenol-red free

DMEM-FBS alone or with the following ligands: 100-300 nM T_3 (L-triiodothyronine), 100 nM LG69 (4-{1-(3,5,5,8,8-pentamethyl-5,6,7,8-tetrahydro-2-napthalenyl)-1-propenyl} benzoic acid), 50-100 nM Am580 (4-(5,6,7,8-tetrahydro-5,5,8,8-tetramethyl-2-napthamido) benzoic acid) or 100 nM VD_3 (1α,25-dihydroxyvitamin D_3). Cells were harvested and assayed for luciferase and ß-galactosidase activity. All points were performed in triplicate in each experiment and varied by less than 10%. Each experiment was repeated three or more times with similar results.

Example 2
Expression and Reporter Constructs

For luciferase assays, response elements with HindIII overhangs were cloned into the HindIII site of the TK-LUC reporter which contains the Herpes virus thymidine kinase promoter (-105/+51). Response elements with the underlined consensus hexanucleotide sequence were as follows:

UAS_G x 4 (i.e., 4 copies of the following sequence):
5'-CGA CGGAGTACTGTCCTCCGAGCT; SEQ ID NO:2

IRO = TREp (i.e., 1 & 2 copies of the following sequence):
5'-TCAGGTCA TGACCTGAG; SEQ ID NO:3

DR4 x 2
5'-AAAGGTCACGAAAGGTCA CCATCCCGGGAAA
AGGTCACGAAAGGTCACC; SEQ ID NO:4

DR5
5'-CAGGTCA-CCAGGAGGTCAGAG; SEQ ID NO:5

DR5 X 2
5'-AAAGGTCACCGAAAGGTCA CCATCCCGGGAAA
AGGTCACCGAAAGGTCACC; SEQ ID NO:6

ER8
5'-TGACCTTTCTCTCC AGGTCA; SEQ ID NO:7

NBRE X 3 (i.e., 3 copies of the following sequence):
5'-GAGTTTAAAAGGTCA TGCTCAATTTTC; SEQ ID NO:8

CRBPII

5'-GTCACAGGTCACAGGTCACAGGTCACAGTTCA; SEQ ID NO:9

MLV-DR4 X 2 (i.e., 2 copies of the following sequence):

5'-AAGGTTCACGAGGTTCACGT; SEQ ID NO:10.

All mammalian expression vectors were derived from pCMX (Umesono et al., 1991, supra) which contains the CMV promoter/enhancer followed by a bacteriophage T7 promoter for transcription *in vitro*. pCMX expression vectors for T_3R_β, hRARα (Umesono et al., 1991, supra) and hRXRα (Yao et al., 1993, supra) were used as previously described. CMX-Nurr1 (provided by Thomas Perlmann), an expression vector for full-length mouse Nurr1, was cloned by inserting the BglII-XhoI fragment from pBS34-1 (excised from λZAP34) (see Law et al., 1992, supra) into pCMX. The VP16-RXR fusion contains the 78 amino acid transactivation domain of Herpes VP16 from pVP16C1 (Novagen) fused N-terminal to the full-length hRXRα.

GAL4 fusions were made by fusing the following receptor ligand binding domains to the C-terminal end of the yeast GAL4 DNA binding domain (amino acids 1-147) from pSG424 (see Sadowski and Ptashne, in *Nucleic Acids Res.* 17:7539 (1989)): human RXRα LBD (Glu 203 - Thr 462); mouse Nurr1 (Cys 318 - Phe 598); human T_3Rß (Leu 173 - Asp 456); human RARα (Glu 156 - Pro 462); and human VDR (Glu 92 - Ser 427). The LBD expression constructs contain the SV40 TAg nuclear localization signal (APKKKRKVG; SEQ ID NO:11) fused upstream of the human T_3Rß LBD (Leu 173 - Asp 456), HRARα LBD (Glu 156 - PRO 462) or the human RXRα LBD (Glu 203 - Thr 462). CMX-ßgal contains the *E. coli* ß-galactosidase coding sequences derived from pCH110 (Pharmacia) cloned into pCMX.

In the left panel of Figure 5, CV-1 cells were transfected with the following plasmids: IRO TK-LUC (300 ng/10^5 cells), CMX-βgal (500 ng/10^5 cells) alone (-) or with

CMX-VP16-RXRα (100 ng/10^5 cells) and/or CMX-hRARα (50 ng/10^5 cells) as indicated. No ligand treatment was employed. Luciferase activity was normalized to the β-galactosidase internal control. In each experiment, the normalized activity obtained in the presence of VP-RXR, T_3R or RAR is plotted as activity relative to the reporter alone, which was defined to have a relative activity of 1.

Example 3
Ligand Binding Assays

Bacterially expressed proteins were used for ligand binding assays. GST-hRXRα (see Mangelsdorf et al., in *Cell* 66:555-561 (1991)), chicken $T_3Rα1$ (see Forman et al., in *Mol. Endocrinol.* 6:429-442 (1992)) and human RARα (Forman et al., 1992, supra) were expressed and purified to near homogeneity as previously described. GST-RXR (150 ng) or a GST control (150 ng) were incubated with or without approximately 500 ng of T_3R or RAR in the presence of 50 nM [^{3}H]-ligands (LG69, 56 Ci/mmol; at-RA, 49 Ci/ mmol; 9-*cis* RA, 29 Ci/mmol), 3 ng/μl poly dI-dC, 50 fmol/μl of the indicated oligonucleotide, 10 μl of 50% (v/v) epoxy-linked glutathione-sepharose (Sigma) in ligand binding buffer (25 mM Tris, pH 7.8, 0.5% CHAPS, 100 mM KCl, 8% Glycerol, 1 mM DTT).

Where indicated (see, for example, Figure 6), unlabeled ligands were added as follows: LG69, 2μM; Am580, 2 μM; T_3, 1 μM. The reaction was mixed for 30 minutes at 25°C and then chilled to 4°C for 10 minutes. The glutathione-sepharose beads were washed three times in ligand binding buffer and the amount of [^{3}H] bound was determined in a liquid scintillation counter. Background binding was determined with the GST control and represented 3-5% of the total binding seen with GST-RXR.

Example 4

RXR Responsiveness is Diminished in T_3R-RXR and RAR-RXR heterodimers

Since T_3R and RAR function as heterodimers with RXR, RXR responsiveness was examined in the context of RXR-T_3R and RXR-RAR heterodimers. Attention is directed to Figure 2, wherein transient transfection analysis of T^3R-RXR and RAR-RXR heterodimers is described. Reporter constructs employed contain the HRE indicated in the figure, cloned upstream of the TK-LUC reporter. In the left panel of the figure, CV-1 cells were transfected with the following plasmids: HRE x 2 - TK-LUC (300 ng/10^5 cells), CMX-h$T_3R\beta$ (20 ng/10^5 cells), CMX-hRXRα (20 ng/10^5 cells) and the internal control CMX-βgal (500 ng/10^5 cells). Cells were treated without ligand or with 100 nM T_3, 100 nM LG69 or 100 nM T_3 + 100 nM LG69.

In the right panel of Figure 2, cells were transfected with HRE x 1 TK-LUC (300 ng/10^5 cells), CMX-hRARα (50 ng/10^5 cells) CMX-hRXRα (50 ng/10^5 cells) and CMX-βgal (500 ng/10^5 cells). Cells were treated without ligand or with 50 nM Am580, 100 nM LG69 or 50 nM Am580 + 100 nM LG69. Normalized luciferase activity was determined and plotted as fold-activation relative to untreated cells.

Although cells transfected with both T_3Rß and RXRα expression vectors were responsive to T_3, they were surprisingly not responsive to the RXR specific ligand LG69 (see Figure 2; Boehm et al., in *J. Med. Chem.* 37:408-414 (1994)). Treatment of these cells with both T_3 and LG69 did not result in further stimulation of the T_3 response, rather the response to T_3 was somewhat reduced. Similarly, cells simultaneously transfected with RARα and RXRα expression vectors responded to the RAR-specific ligand Am580, but remained unresponsive to LG69. In contrast, treatment with

Am580 + LG69 resulted in increased transcriptional activity over that seen with AM580 alone.

Example 5
Suppression of RXR Activity is Mediated by the LBD

Since RXR homodimers are activated RXR agonists, the results presented above suggest that RXR activity is suppressed in unliganded RXR-T_3R and RXR-RAR heterodimers. It is suspected that heterodimerization within the LBD (see Figure 1) could induce an allosteric change in the RXR LBD that blocks its ability to bind ligand and/or transactivate. To test this hypothesis, a system was developed to examine the responsiveness of RXR-containing heterodimers in a manner that relies solely on interactions between the LBDs.

Thus, a chimeric protein was constructed containing the yeast GAL4 DBD linked to the RXR LBD (GAL-RXR). The ability of this RXR-chimera to respond to LG69 was initially examined in the presence of truncated receptors containing the LBDs of T_3R or RAR. Thus, transient transfection analysis of GAL-RXR LBD was carried out in the presence of T_3R, RAR or VDR LBDs. Reporter constructs contained 4 copies of the UAS_G cloned upstream of the TK-LUC reporter. CV-1 cells were tranfected with UAS_G X 4 TK-LUC (300 ng/10^5 cells), CMX-GAL-RXR (100 ng/10^5 cells), CMX-βgal (500 ng/10^5 cells) alone or with either CMX-T_3R LBD, CMX-RAR LBD or CMX-VDR LBD (100 ng/10^5 cells). Following transfection, cells were treated without ligand or with 100 nM LG69, 100 nM T_3, 50 nM Am580 or 100 nM VD_3. Normalized luciferase activity was determined and plotted as reporter activity (see Figure 3).

Although GAL-RXR activated the UAS_G reporter in response to LG69, the absolute levels of induced and uninduced activity were dramatically suppressed by both T_3R

and RAR LBDs (see Figure 3). In contrast, the VDR LBD failed to suppress RXR responsiveness. These results indicate that suppression of RXR by unliganded T_3R and RAR is mediated solely by interactions between the LBDs of these receptors.

These results are consistent with previous experiments which have shown that receptor LBDs remain tethered to the GAL-RXR LBD in cells (see, for example, Nagpal et al., 1993, supra). Thus, it was next sought to determine whether the tethered LBDs can activate transcription in response to their specific ligands. As seen in Figure 3, the T_3R, RAR and VDR LBDs conferred ligand-dependent activation upon GAL-RXR, but not GAL4 alone. Thus, receptor LBDs tethered to RXR provide all the functions required for ligand-dependent transcriptional activation in the absence of direct DNA contact.

The experiment described with respect to Figure 3 was also performed with the combination of RXR-specific ligand (e.g., LG69) and T_3R or RAR specific ligand (see Figure 4, which illustrates the differential modulation of RXR transcriptional activity by the LBD of T_3R. Thus, cells treated according to the procedure described above with respect to Figure 3 were additionally treated with 100 nM T_3 + 100 nM LG69 (see Figure 4A) or 50 nM AM580 + 100 nM LG69 (see Figure 4B). Normalized luciferase activity was determined and plotted as fold-activation relative to untreated cells.

In order to compare the effects of T_3R and RAR LBDs on LG69 inducibility of GAL-RXR, these data were re-plotted as fold-induction. Comparison of Figures 2 and 4 indicate that the effects of ligand-occupied T_3R and RAR are qualitatively similar, regardless of whether the full-length receptors or their LBDs are used. Note that the T_3R LBD led to a coordinate reduction in both basal and LG69-

induced activities of GAL-RXR, hence the fold response to LG69 was only modestly inhibited from 69-fold (see Figure 4A, GAL-RXR alone) to 57-fold by the T_3R LBD (Figure 4B, GAL-RXR + T_3R LBD). Addition of T_3 resulted in strong activation of T_3R and the combination of T_3 + LG69 resulted in slightly less activity than with T_3 alone. In contrast to T_3R, unliganded RAR LBD strongly suppressed the fold-responsiveness of GAL-RXR to LG69. Treatment with Am580 + LG69 resulted in increased transcriptional activity over that seen with AM580 alone suggesting that RXR responsiveness to LG69 may be restored by addition of the RAR agonist Am580 (Figure 4B).

Example 6
RAR and T_3R Differentially Suppress the Ligand Binding Activity of RXR

In addition to decreasing basal and activated transcription, RAR also blocks the ability of RXR to respond to its ligand. Thus, the possibility that RXR is incapable of binding ligand when tethered to RAR was examined. A bacterially expressed glutathione-S-transferase-RXRa fusion protein (GST-RXR) was incubated with recombinant T_3R or RAR in the presence of radiolabeled RXR ligands. The amount of ligand bound to RXR or RXR-containing heterodimers was quantitated using glutathione-sepharose as an affinity probe. In the left panel of Figure 6A, purifed GST-hRXRα was incubated with 50 nM [^{3}H]LG69 (56 Ci/mmol) and the optimized RAR reponse element 5'-GCAAA AGGTCA AAAAG AGGTCA TGC-3'; SEQ ID NO:12; Kurokawa et al., *Genes Dev.* 7:1423-1435 (1993)) alone or with 2 μM LG69, 2μM Am580. In the right panel of Figure 6A, purified GST-hRXRα and the RAR response element were incubated with 25 nM [^{3}H]at-RA (49 Ci/mmol) without or with 500 ng of hRARα. The amount of specifically bound [^{3}H]label was then determined employing standard techniques as previously described.

As expected, binding of [^{3}H]LG69 to GST-RXR was specifically completed by unlabeled LG69, but not by the RAR-specific ligand Am580 (see Figure 6A, right panel); specific binding of [^{3}H]all-trans RA (at-RA) was observed when GST-RXR was mixed with excess RAR (see Figure 6A, right panel). A quantitation of the amount of specifically bound [^{3}H]LG69, [^{3}H]at-RA or [^{125}I]T_3 indicates that GST-RXR could be saturated with approximately equimolar amounts of RAR or T_3R, respectively. Electrophoretic mobility shift experiments indicate that ligands do not alter the binding activity of T_3R-RXR or RAR-RXR heterodimers.

Next, the ligand binding activity of RXR was examined in the presence of RAR-T_3R. Thus, purified GST-hRXRα and 50 nM [^{3}H]LG69 (56 Ci/mmol) were incubated alone or with 500 ng of hRARα or chicken $T_3R\alpha 1$ and the optimized RAR response element or the optimized T_3R response element 5'-GCAAA AGGTCA AATA AGGTCA CGT-3'; SEQ ID NO:13; Kurokawa et al., supra), respectively. Where indicated, unlabeled T_3 was added to a concentration of 1 μM. Specifically bound [^{3}H]LG69 was determined.

Surprisingly, addition of RAR resulted in a dramatic (<85%) decrease in the amount of [^{3}H]LG69 bound to GST-RXR (see Figure 6B), indicating that the ligand binding potential of RXR is reduced in the RXR-RAR heterodimer. These findings account for the ability of unoccupied RAR to suppress the ligand inducibility of RXR (see Figure 4B).

Similar experiments were performed on the RXR-T_3R heterodimer. In contrast to RAR, unliganded T_3R led to a modest reduction in [^{3}H]LG69 binding. However, ligand binding was strongly diminished upon addition of T_3 (Figure 6B). These findings are consistent with the observation that unoccupied T_3R results in a modest suppression of RXR inducibility, whereas no induction is elicited when T_3R is occupied by T_3 (Figure 4B).

The transfection experiments summarized in Figures 2 and 4B indicate that RAR-RXR heterodimers exhibit RXR responsiveness only in the presence of an RAR ligand, suggesting that RXR binding activity may be restored by RAR ligands. To test this hypothesis, the observation that 9-*cis* RA binds with high affinity to both RAR and RXR (Allegretto et al., 1993; Allenby et al., 1993) was applied as follows. Thus, GST-RXR/RAR heterodimers were allowed to form in the presence of [^{3}H]9-*cis* RA. Reactions were performed as described above with reference to Figure 6A, using both GST-hRXRα and hRARα with 50 nM [^{3}H]9-cis RA (29 Ci/mmol). Specifically bound [^{3}H]9-cis RA was determined in the absence or presence of 2 μM LG69 and/or 2 μM Am580. In all experiments, maximal binding was in the range of 200-300 fmol of [^{3}H]ligand.

Although Am580 fully competed with [^{3}H]at-RA for binding to GST-RXR/RAR heterodimers (Figure 6A, right panel), Am580 resulted in only a partial decrease in [^{3}H]9-*cis* RA binding (see Figure 6C). Nearly complete competition was observed by addition of both Am580 and the RXR-specific ligand LG69 (see Figure 6C), suggesting that RXR can bind ligand, provided the RAR LBD is occupied. These findings are consistent with the restoration of RXR responsiveness in RAR-occupied heterodimers (Figure 4B).

Example 7

Identification of a Novel RXR-permissive Heterodimer

Since RXR serves as a silent partner in the T_3R and RAR pathways, it was next investigated whether RXR could serve as an active component in other complexes. To search for such complexes, the LBD of a number of nuclear receptors were fused to the GAL4 DBD, and tested to determine whether the RXR LBD could confer LG69 responsiveness upon these GAL-LBD chimeras. Thus, CV-1 cells were transfected with UAS_9 x 4 TK-LUC (300 ng/10^5

cells), CMX-βgal (500 ng/10^5 cells) and the indicated CMX-GAL-receptor LBD construct (100 ng/10^5 cells) with or without CMX-RXR LBD (100 ng/10^5 cells). Following transfection, cells were treated without ligand or with 100 nM LG69. Normalized luciferase activity was determined and plotted as fold-activation relative to untreated cells.

As expected, LG69 responsiveness was not seen when the RXR LBD was expressed alone, or with GAL-T_3R and GAL-RAR (see Figure 7A). Similarly, LG69 inducibility was not observed with chimeras containing the LBDs of VDR (see Figure 7A) or several other members of the nuclear receptor superfamily. Unexpectedly, strong responsiveness to LB69 was observed when the RXR-LBD was co-expressed with a GAL-Nurr1 chimera (see Figure 7A). These results suggest that the LBDs of Nurr1 and RXR form a novel heterodimer complex which promotes potent RXR responsiveness.

Nurr1 (also known as RNR-1, NOT, HZF-3), the β isoform of NGFI-b (also known as nur77, N10, NAK-1, TR3), is reported to be a constitutively active orphan receptor that binds as a high-affinity monomer to an AA-AGGTCA core-site (NBRE) (see, for example, Law et al., 1992, supra; Wilson et al., 1992, supra; Scearce et al., 1993, supra; and Wilson et al., 1993, supra). This prompted further investigation as to whether full-length Nurr1 and RXR could interact productively on the NBRE.

Thus, CV-1 cells were tranfected with NBRE x 3 TK-LUC (300 ng/10^5 cells), CMX-βgal (500 ng/10^5 cells), alone or with CMX-Nurr1 (100 ng/10^5 cells) and CMX-hRXRα (100 ng/10^5 cells) as indicated in Figure 7B. Following transfection, cells were treated with or without 100 nM LG69. Normalized luciferase activity was determined and plotted as reporter activity.

Consistent with published results (see, for example, Scearce et al., 1993, supra), Nurr1 constitutively activates the NBRE reporter (see Figure 7B), but was not responsive to LG69 (Figure 7B). RXR, which does not bind to the NBRE, did not activate this reporter. However, when Nurr1 and RXR are co-expressed, the constitutive activity of Nurr1 is suppressed, and the complex becomes strongly responsive to LG69 (Figure 7B). Similar results were obtained with RXRα, RXRß and RXRγ.

LIGAND.

The ability of the Nurr1-RXR heterodimer complex to transduce RXR signals suggested the desirability of comparing the activity of this complex with that of RXR on an established RXR response element (CRBPII, cellular retinol binding protein II; see Mangelsdorf et al., 1991, supra). Using sub-optimal amounts of RXR-expression vector, the CRBPII reporter was compared with a 3-copy NBRE reporter as follows. Cells were transfected as described with respect to Figure 7B, but with a 5-fold lower amount of CMX-hRXRα (20 ng/10^5 cells). CRBPII TK-LUC (300 ng/10^5 cells) was used where indicated.

Since RXR was limiting in this assay, only minimal activation of the CRBPII reporter was observed (see Figure 7C). In contrast, Nurr1-RXR displayed a potent response to LG69, despite the fact that the NBRE reporter contains 1 less core-binding site than CRBPII (see Figure 7C). Thus, Nurr1-RXR can efficiently transduce RXR signals. However, unlike other heterodimers, the Nurr1-RXR complex is strongly responsive to LG69 and 9-*cis* RA, suggesting that this complex establishes a novel signaling pathway for 9-*cis* RA.

Example 8

Nurr1 Does not Require the RXR DBD for Coupling

The Nurr1-RXR complex is unique in several ways. First, the Nurr1 DBD recognizes its response element in the absence of RXR (see, for example, Wilson et al., 1992, supra; Scearce et al., 1993, supra; and Wilson et al., 1993, supra). Second, the monovalent NBRE serves as a response element for a multimeric Nurr1-RXR complex (see Figure 7B). These observations raise the possibility that RXR associates with NBRE-bound Nurr1 in the absence of RXR-specific DNA contacts. Such behavior would be in sharp contrast with T_3R, RAR and VDR, which rely on RXR-specific contacts to recognize hormone response elements. Indeed, RXR mutants lacking the DBD associate with wild-type RAR; however, these complexes do not bind DNA or activate transcription (see Minucci et al., in *Mol. Cell Biol.* 14:360-372 (1994)).

This prompted an investigation of the question of whether the RXR DBD is required for activation through the Nurr1 pathway. Thus, CV-1 cells were transfected with TK-LUC reporters (300 ng/10^5 cells), CMX-βgal (500 ng/10^5 cells) and the indicated CMX-receptor construct (20 ng/10^5 cells; see Figure 7D) with or without CMX-RXR-LBD (100 ng/10^5 cells). The following receptor, reporter, ligand combinations were used: Nurr1, NBRE x 3, 100 nM LG69; h$T_3R\beta$, MLV x 2, 100 nM T_3; hRARα, DR5 x 2, 100 nM Am580; hVDR, SPP1 x 3, 100 nM VD_3. Normalized luciferase activity was determined and plotted as percent of maximal fold-activation where 100% is defined as the fold activation by T_3R, RAR, VDR, the RXR LBD, or Nurr1 + RXR LBD. The actual fold-activation values are shown above each bar in the figure.

As shown in Figure 7D, the RXR LBD is sufficient to confer strong LG69 responsiveness upon Nurr1. In

contrast, the RXR LBD acts as a dominant-negative inhibitor of wild-type VDR, T_3R and RAR (Figure 7D). These findings indicate that the RXR DBD is not required for ligand-dependent activation of Nurr1-RXR, a property that further distinguishes this novel complex from previously described RXR-containing complexes.

While the invention has been described in detail with reference to certain preferred embodiments thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Forman, Barry M.
Umesono, Kazuhiko

(ii) TITLE OF INVENTION: ALLOSTERIC CONTROL OF NUCLEAR HORMONE RECEPTORS

(iii) NUMBER OF SEQUENCES: 13

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/372,217
(B) FILING DATE: 13-JAN-1995
(C) CLASSIFICATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
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Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
        35                  40                  45
```

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
50 55 60

Lys Cys Xaa Xaa Xaa Gly Met
65 70

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGACGGAGTA CTGTCCTCCG AGCT 24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCAGGTCATG ACCTGAG 17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGGTCACG AAAGGTCACC ATCCCGGGAA AAGGTCACGA AAGGTCACC 49

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAAGGTCACC GAAAGGTCAC CATCCCGGGA AAAGGTCACC GAAAGGTCAC C 51

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGACCTTTCT CTCCAGGTCA 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTTTAAAA GGTCATGCTC AATTTTC 27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCACAGGTC ACAGGTCACA GGTCACAGTT CA 32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGGTTCACG AGGTTCACGT 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Pro Lys Lys Lys Arg Lys Val Gly
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAAAGGTC AAAAAGAGGT CATGC 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCAAAAGGTC AAATAAGGTC ACGT 24

That which is claimed is:

1. A heterodimer complex comprising RXR and a silent partner therefor.

2. A heterodimer complex according to claim 1 wherein said silent partner is an isoform of Nurr1.

3. A heterodimer complex according to claim 1 wherein RXR is selected from RXRα, RXRβ or RXRγ.

4. A heterodimer complex according to claim 3 wherein RXR is RXRα.

5. A heterodimer complex according to claim 3 wherein RXR is RXRβ.

6. A heterodimer complex according to claim 3 wherein RXR is RXRγ.

7. A method to suppress the constitutive activity of Nurr1, said method comprising contacting Nurr1 with at least the ligand binding domain of RXR.

8. A method according to claim 7 wherein the ligand binding domain of RXR is selected from RXRα, RXRβ or RXRγ.

9. A method to render Nurr1-containing cells inducibly responsive to RXR selective ligands, said method comprising contacting said cells with at least the ligand binding domain of RXR.

10. A method according to claim 9 wherein the ligand binding domain of RXR is selected from RXRα, RXRβ or RXRγ.

11. A method to render RXR-containing cells responsive to RXR selective ligands, said method comprising contacting said cells with a silent partner therefor.

12. A method according to claim 11, wherein said silent partner is an isoform of Nurr1.

13. A method for the identification of nuclear receptor(s) which participate as silent partner(s) in the formation of a heterodimer with RXR, said method comprising

introducing into a cell:

at least the ligand binding domain of a putative silent partner for RXR,

a chimeric construct containing a GAL4 DNA binding domain and at least the ligand binding domain of RXR, and

a reporter construct, wherein said reporter construct comprises:

(a) a promoter that is operable in said cell,

(b) a GAL4 response element, and

(c) DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said GAL4 response element is operatively linked to said promoter for activation thereof, and thereafter

monitoring expression of reporter upon exposure of the above-described cell to RXR selective ligand(s).

14. A method for the identification of nuclear receptor(s) which participate as silent partner(s) in the formation of heterodimer(s) with RXR, said method comprising

introducing into a cell:
a putative silent partner for RXR,
at least the ligand binding domain of RXR, and
a reporter construct, wherein said reporter construct comprises:
(a) a promoter that is operable in said cell,
(b) a response element for said putative silent partner, and
(c) DNA encoding a reporter protein,
wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and
wherein said response element for said putative silent partner is operatively linked to said promoter for activation thereof, and thereafter

monitoring expression of reporter upon exposure of the above-described cell to RXR selective ligand(s).

15. A method according to claim 14 wherein the response element for the putative silent partner has the sequence AAAGGTCA.

IR-10 Separate

16. A method for identifying ligands selective for heterodimers comprising RXR and a silent partner therefor, said method comprising

comparing the level of expression of reporter when cells containing a reporter construct, RXR and silent partner therefor are exposed to test compound, relative to the level of expression of reporter when cells containing a reporter construct, RXR and a member of the steroid/thyroid superfamily which is not a silent partner therefor are exposed to test compound, and

selecting those compounds which activate only the combination of RXR and silent partner therefor.

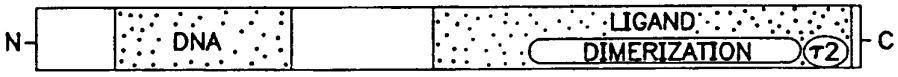


FIG. 1

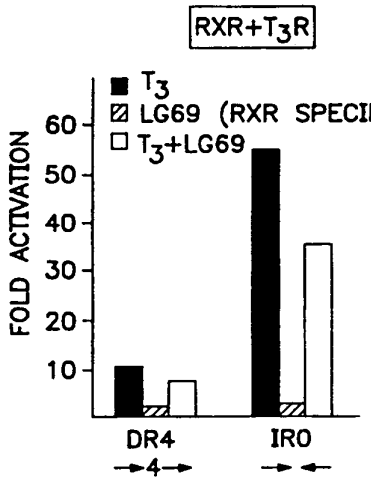

RXR+T3R
T3
LG69 (RXR SPECIFIC)
T3+LG69
FOLD ACTIVATION
60
50
40
30
20
10
DR4
4
IR0

FIG. 2A

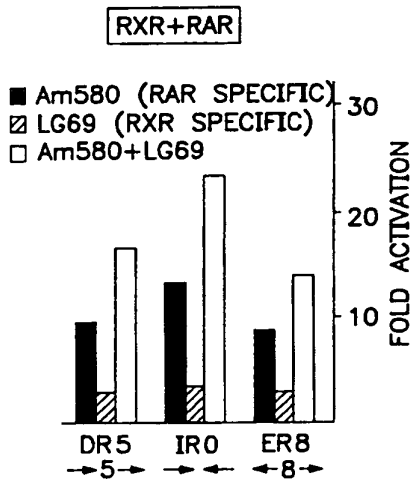

RXR+RAR
Am580 (RAR SPECIFIC)
LG69 (RXR SPECIFIC)
Am580+LG69
FOLD ACTIVATION
30
20
10
DR5
5
IR0
ER8
8

FIG. 2B

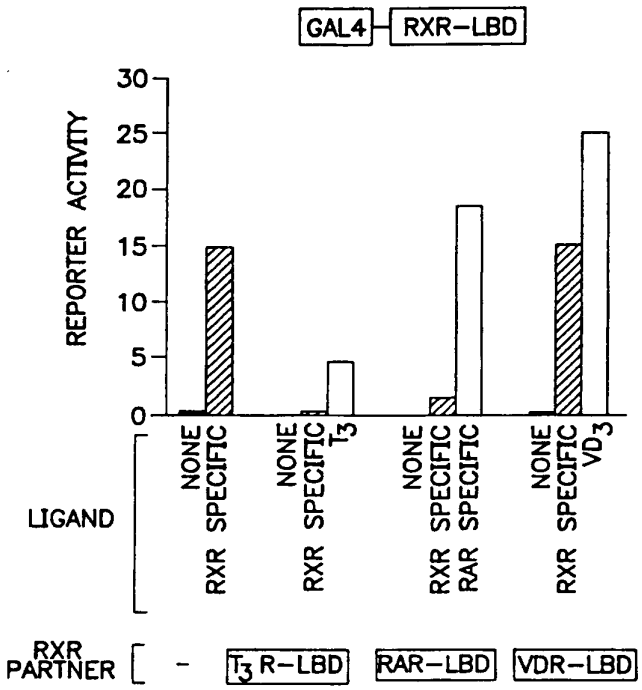

GAL4
RXR-LBD
REPORTER ACTIVITY
30
25
20
15
10
5
0
LIGAND
NONE
RXR SPECIFIC
NONE
RXR SPECIFIC
T3
NONE
RXR SPECIFIC
RAR SPECIFIC
NONE
RXR SPECIFIC
VD3
RXR PARTNER
-
T3 R-LBD
RAR-LBD
VDR-LBD

FIG. 3

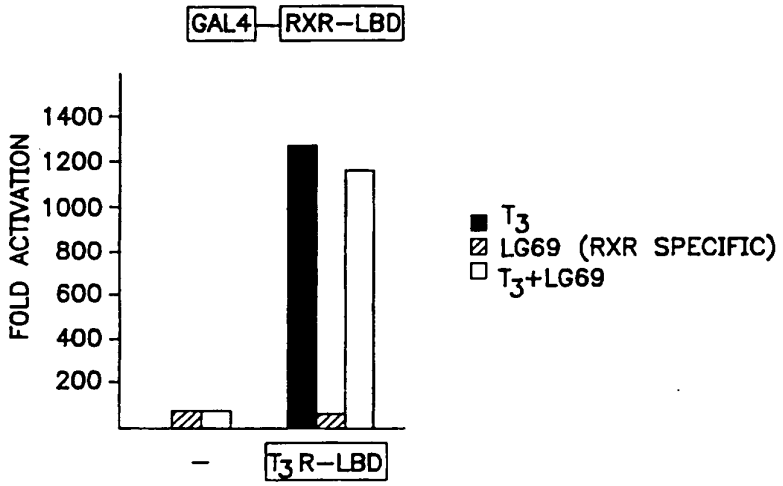

GAL4
RXR-LBD
FOLD ACTIVATION
1400
1200
1000
800
600
400
200
T3
LG69 (RXR SPECIFIC)
T3+LG69
-
T3R-LBD

FIG. 4A

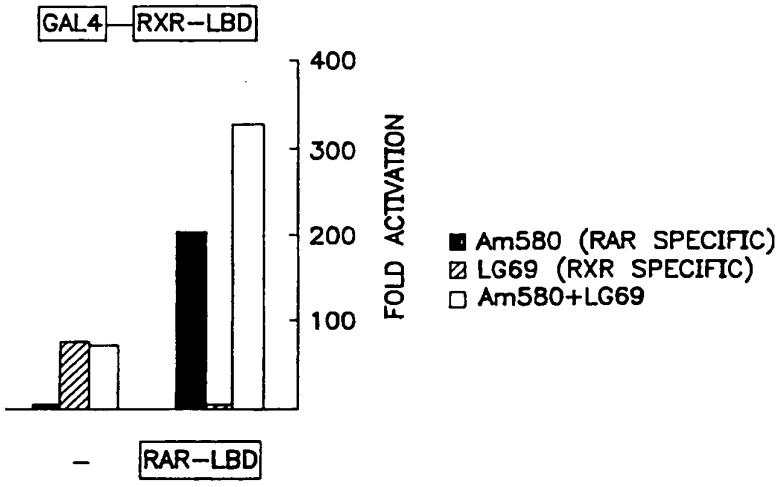

GAL4
RXR-LBD
400
300
200
100
FOLD ACTIVATION
Am580 (RAR SPECIFIC)
LG69 (RXR SPECIFIC)
Am580+LG69
-
RAR-LBD

FIG. 4B

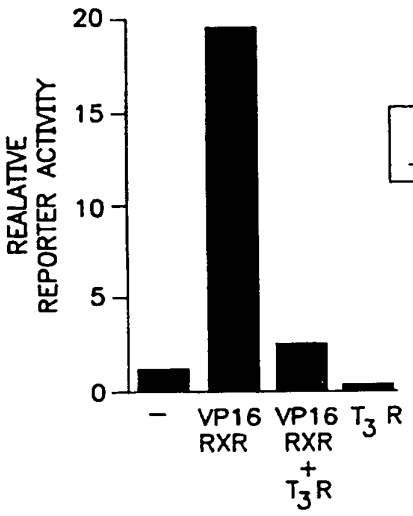

REALATIVE
REPORTER ACTIVITY
20
15
10
5
0
IRO
–
VP16
RXR
VP16
RXR
+
T_3R
T_3 R

FIG. 5A

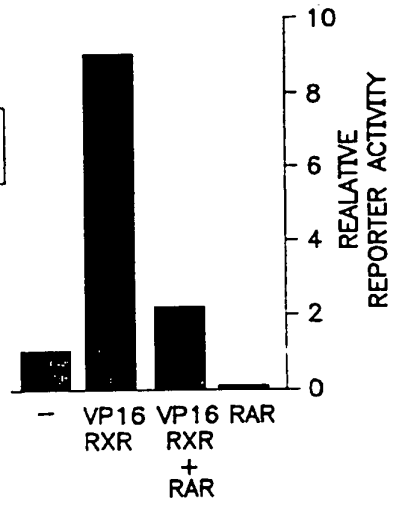

10
8
6
4
2
0
REALATIVE
REPORTER ACTIVITY
–
VP16
RXR
VP16
RXR
+
RAR
RAR

FIG. 5B

FIG. 6A

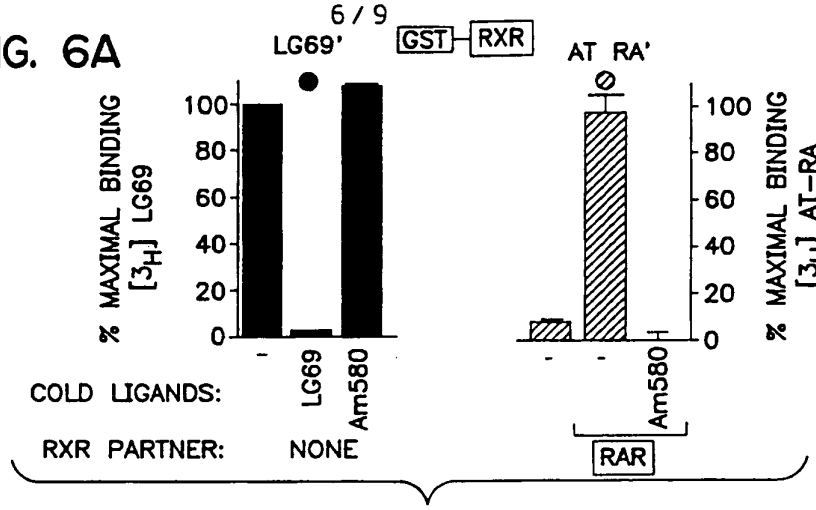


FIG. 6B

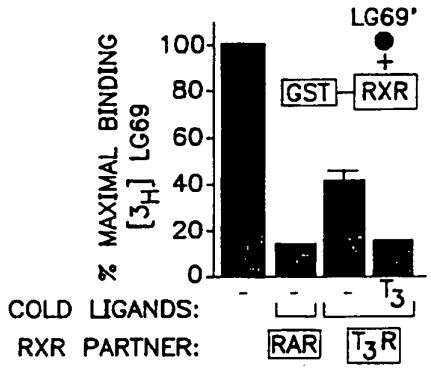
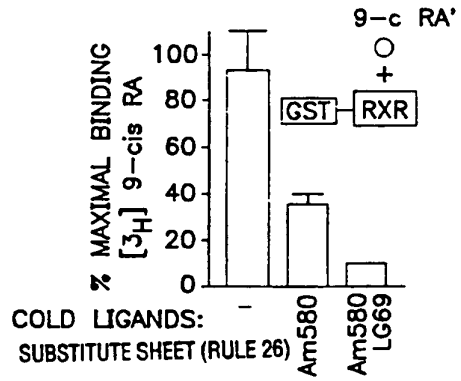


FIG. 6C



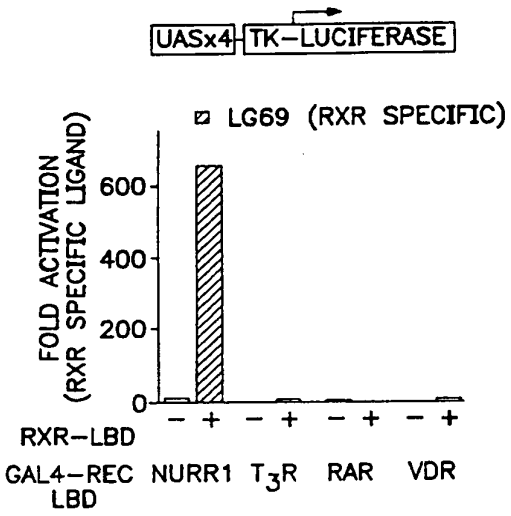

UASx4
TK–LUCIFERASE
LG69 (RXR SPECIFIC)
FOLD ACTIVATION (RXR SPECIFIC LIGAND)
600
400
200
0
– + – + – + – +
RXR–LBD
GAL4–REC LBD
NURR1
T3R
RAR
VDR

FIG. 7A

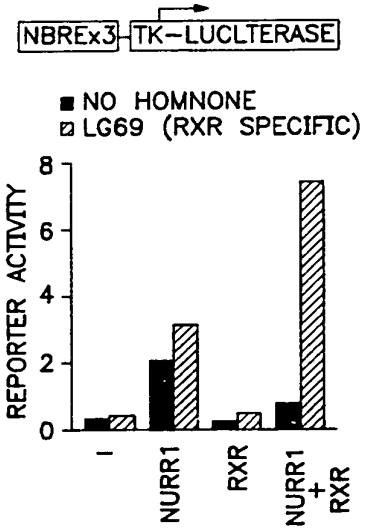

NBREx3
TK–LUCLTERASE
NO HOMNONE
LG69 (RXR SPECIFIC)
REPORTER ACTIVITY
8
6
4
2
0
–
NURR1
RXR
NURR1 + RXR

FIG. 7B

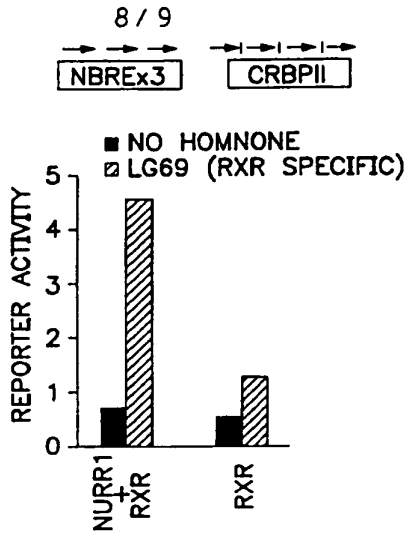

NBREx3
CRBPII
NO HOMNONE
LG69 (RXR SPECIFIC)
REPORTER ACTIVITY
0
1
2
3
4
5
NURR1 + RXR
RXR

FIG. 7C

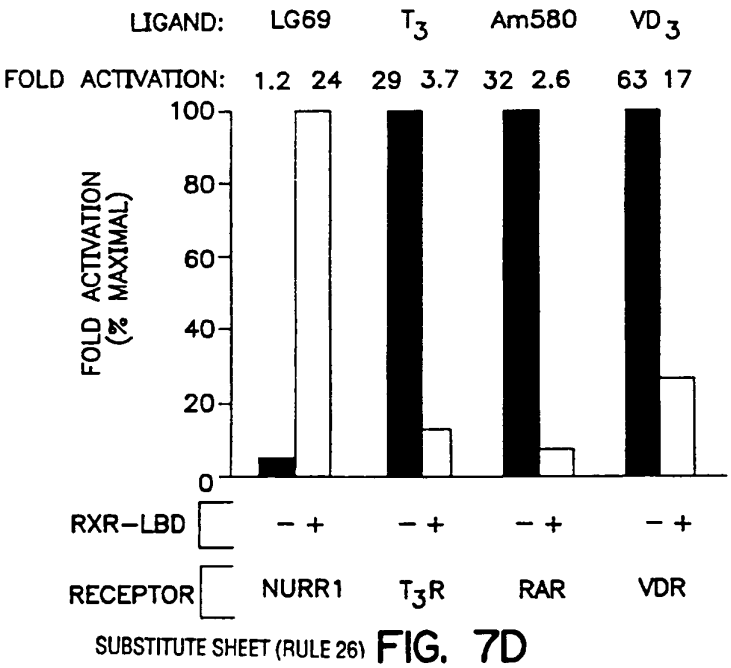

LIGAND: LG69 T3 Am580 VD3
FOLD ACTIVATION: 1.2 24 29 3.7 32 2.6 63 17
FOLD ACTIVATION (% MAXIMAL)
0
20
40
60
80
100
RXR-LBD - + - + - + - +
RECEPTOR NURR1 T3R RAR VDR

 FIG. 7D

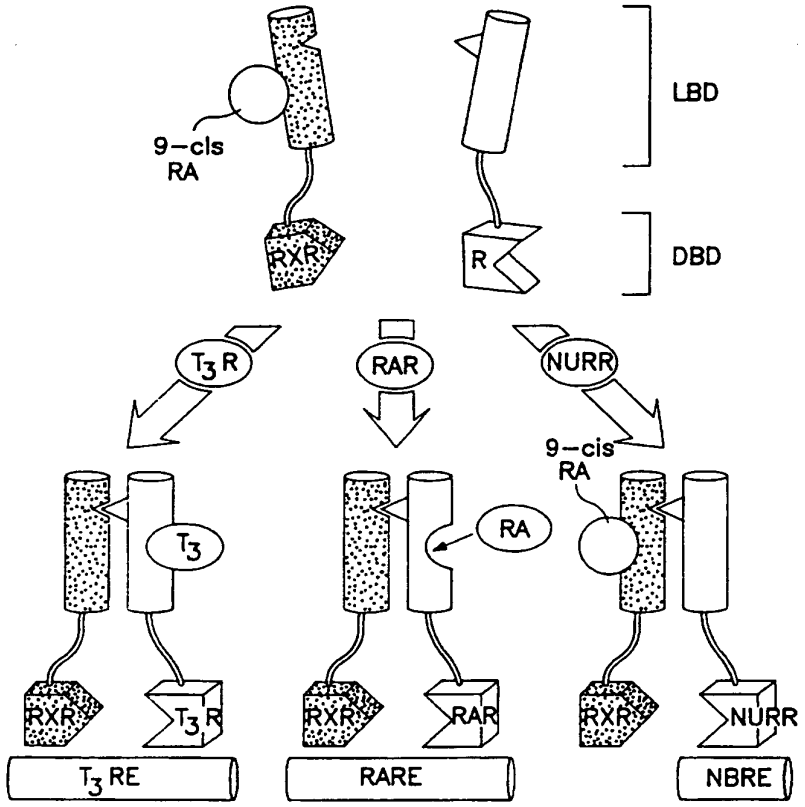

9-cis
RA
RXR
R
LBD
DBD
T3 R
RAR
NURR
9-cis
RA
T3
RA
RXR
T3 R
RXR
RAR
RXR
NURR
T3 RE
RARE
NBRE

FIG. 8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/17024

A. CLASSIFICATION OF SUBJECT MATTER
IPC(6) :A61K 38/17; C07K 14/705; C12N 15/79; G01N 33/68
US CL :435/7.21, 69.1, 240.2; 514/2; 530/350
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.21, 69.1, 240.2; 514/2; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, EMBASE, SCISEARCH, MEDLINE search terms: RXR, retinoic acid receptor, nurr1, RNR-1, NAK1, "NOT", NGFB-1, Nur77, heterodimer, complex, conjugate

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P ----- Y, P	GENES & DEVELOPMENT, Volume 9, issued February 1995, Perlmann et al, "A novel pathway for vitamin A signaling mediated by RXR heterodimerization with NGFI-B and NURR1", pages 769-782, see pages 770-779.	1-4, 7-16 ---------- 5, 6
Y	THE JOURNAL OF BIOLOGICAL CHEMISTRY, Volume 268, Number 12, issued 25 April 1993, Scearce et al, "RNR-1, a Nuclear Receptor in the NGFI-B/Nur77 Family That Is Rapidly Induced in Regenerating Liver", pages 8855-8861, see page 8855.	1, 2
Y	MOLECULAR ENDOCRINOLOGY, Volume 6, Number 12, issued 1992, Law et al, "Identification of a New Brain-Specific Transcription Factor, NURR1", pages 2129-2135, see page 2129.	1, 2

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
07 MARCH 1996	20 MAR 1996
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer KEN SORENSEN Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*